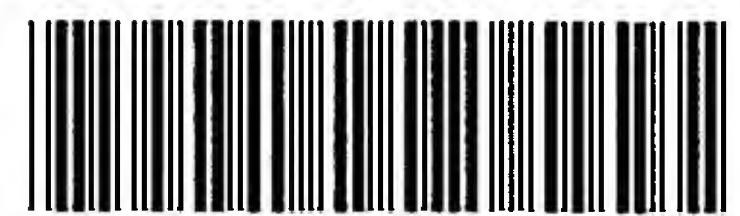


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/604,340 A
Source: 1600-EFS
Date Processed by STIC: 7-15-05

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/604,340A

DATE: 07/15/2005

TIME: 08:17:01

Input Set : N:\efs\10604340A_efs\RNAi_seq_ST25.txt
 Output Set: N:\CRF4\07152005\J604340A.raw

3 <110> APPLICANT: Hildinger, Markus
 5 <120> TITLE OF INVENTION: Decreasing gene expression in a mammalian subject in vivo
 via
 6 AAV-mediated RNAi expression cassette transfer
 8 <130> FILE REFERENCE: 2
 10 <140> CURRENT APPLICATION NUMBER: US 10/604,340A
 11 <141> CURRENT FILING DATE: 2003-07-13
 13 <160> NUMBER OF SEQ ID NOS: 12
 15 <170> SOFTWARE: PatentIn version 3.2
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 6437
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: sequence for recombinant adeno-associated viral vector,
 including
 24 plasmid backbone, with AAV2 internal terminal repeats that flank
 25 expression cassette; referred to as AAV2/2 CMV luciferase
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1228)..(2883)
 31 <223> OTHER INFORMATION: luciferase cDNA
 33 <400> SEQUENCE: 1
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 70 agtatacaagg ttacaagaca ggttaagga gaccaataga aactgggctt gtcgagacag 1140
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 74 ctctccacag gtgtccaggc ggccgcc atg gaa gac gcc aaa aac ata aag aaa 1254

75

Met Glu Asp Ala Lys Asn Ile Lys Lys

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Output Set: N:\CRF4\07152005\J604340A.raw

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82 ctg cat aag gct atg aag aga tac gcc ctg gtt cct gga aca att gct			1350
83 Leu His Lys Ala Met Lys Arg Tyr Ala Leu Val Pro Gly Thr Ile Ala			
84 30 35 40			
86 ttt aca gat gca cat atc gag gtg gac atc act tac gct gag tac ttc			1398
87 Phe Thr Asp Ala His Ile Glu Val Asp Ile Thr Tyr Ala Glu Tyr Phe			
88 45 50 55			
90 gaa atg tcc gtt cggtt gca gaa gct atg aaa cga tat ggg ctg aat			1446
91 Glu Met Ser Val Arg Leu Ala Glu Ala Met Lys Arg Tyr Gly Leu Asn			
92 60 65 70			
94 aca aat cac aga atc gtc gta tgc agt gaa aac tct ctt caa ttc ttt			1494
95 Thr Asn His Arg Ile Val Val Cys Ser Glu Asn Ser Leu Gln Phe Phe			
96 75 80 85			
98 atg ccg gtg ttg ggc gcg tta ttt atc gga gtt gca gtt gcg ccc gcg			1542
99 Met Pro Val Leu Gly Ala Leu Phe Ile Gly Val Ala Val Ala Pro Ala			
100 90 95 100 105			
102 aac gac att tat aat gaa cgt gaa ttg ctc aac agt atg ggc att tcg			1590
103 Asn Asp Ile Tyr Asn Glu Arg Glu Leu Leu Asn Ser Met Gly Ile Ser			
104 110 115 120			
106 cag cct acc gtg gtg ttc gtt tcc aaa aag ggg ttg caa aaa att ttg			1638
107 Gln Pro Thr Val Val Phe Val Ser Lys Lys Gly Leu Gln Lys Ile Leu			
108 125 130 135			
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111 Asn Val Gln Lys Lys Leu Pro Ile Ile Gln Lys Ile Ile Ile Met Asp			
112 140 145 150			
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115 Ser Lys Thr Asp Tyr Gln Gly Phe Gln Ser Met Tyr Thr Phe Val Thr			
116 155 160 165			
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119 Ser His Leu Pro Pro Gly Phe Asn Glu Tyr Asp Phe Val Pro Glu Ser			
120 170 175 180 185			
122 ttc gat agg gac aag aca att gca ctg atc atg aac tcc tct gga tct			1830
123 Phe Asp Arg Asp Lys Thr Ile Ala Leu Ile Met Asn Ser Ser Gly Ser			
124 190 195 200			
126 act ggt ctg cct aaa ggt gtc gct ctg cct cat aga act gcc tgc gtg			1878
127 Thr Gly Leu Pro Lys Gly Val Ala Leu Pro His Arg Thr Ala Cys Val			
128 205 210 215			
130 aga ttc tcg cat gcc aga gat cct att ttt ggc aat caa atc att ccg			1926
131 Arg Phe Ser His Ala Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro			
132 220 225 230			
134 gat act gcg att tta agt gtt gtt cca ttc cat cac ggt ttt gga atg			1974
135 Asp Thr Ala Ile Leu Ser Val Val Pro Phe His His Gly Phe Gly Met			
136 235 240 245			
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139 Phe Thr Thr Leu Gly Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met			
140 250 255 260 265			

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143 Tyr Arg Phe Glu Glu Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr Lys	
144 270 275 280	
146 att caa agt gcg ctg ctg gtg cca acc cta ttc tcc ttc gcc aaa	2118
147 Ile Gln Ser Ala Leu Leu Val Pro Thr Leu Phe Ser Phe Phe Ala Lys	
148 285 290 295	
150 agc act ctg att gac aaa tac gat tta tct aat tta cac gaa att gct	2166
151 Ser Thr Leu Ile Asp Lys Tyr Asp Leu Ser Asn Leu His Glu Ile Ala	
152 300 305 310	
154 tct ggt ggc gct ccc ctc tct aag gaa gtc ggg gaa gcg gtt gcc aag	2214
155 Ser Gly Gly Ala Pro Leu Ser Lys Glu Val Gly Glu Ala Val Ala Lys	
156 315 320 325	
158 agg ttc cat ctg cca ggt atc agg caa gga tat ggg ctc act gag act	2262
159 Arg Phe His Leu Pro Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr	
160 330 335 340 345	
162 aca tca gct att ctg att aca ccc gag ggg gat gat aaa ccg ggc gcg	2310
163 Thr Ser Ala Ile Leu Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala	
164 350 355 360	
166 gtc ggt aaa gtt gtt cca ttt ttt gaa gcg aag gtt gtg gat ctg gat	2358
167 Val Gly Lys Val Val Pro Phe Phe Glu Ala Lys Val Val Asp Leu Asp	
168 365 370 375	
170 acc ggg aaa acg ctg ggc gtt aat caa aga ggc gaa ctg tgt gtg aga	2406
171 Thr Gly Lys Thr Leu Gly Val Asn Gln Arg Gly Glu Leu Cys Val Arg	
172 380 385 390	
174 ggt cct atg att atg tcc ggt tat gta aac aat ccg gaa gcg acc aac	2454
175 Gly Pro Met Ile Met Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn	
176 395 400 405	
178 gcc ttg att gac aag gat gga tgg cta cat tct gga gac ata gct tac	2502
179 Ala Leu Ile Asp Lys Asp Gly Trp Leu His Ser Gly Asp Ile Ala Tyr	
180 410 415 420 425	
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183 Trp Asp Glu Asp Glu His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu	
184 430 435 440	
186 att aag tac aaa ggc tat cag gtg gct ccc gct gaa ttg gaa tcc atc	2598
187 Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Ser Ile	
188 445 450 455	
190 ttg ctc caa cac ccc aac atc ttc gac gca ggt gtc gca ggt ctt ccc	2646
191 Leu Leu Gln His Pro Asn Ile Phe Asp Ala Gly Val Ala Gly Leu Pro	
192 460 465 470	
194 gac gat gac gcc ggt gaa ctt ccc gcc gcc gtt gtt ttg gag cac	2694
195 Asp Asp Asp Ala Gly Glu Leu Pro Ala Ala Val Val Leu Glu His	
196 475 480 485	
198 gga aag acg atg acg gaa aaa gag atc gtg gat tac gtc gcc agt caa	2742
199 Gly Lys Thr Met Thr Glu Lys Glu Ile Val Asp Tyr Val Ala Ser Gln	
200 490 495 500 505	
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203 Val Thr Thr Ala Lys Lys Leu Arg Gly Gly Val Val Phe Val Asp Glu	
204 510 515 520	
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211	Ile Leu Ile Lys Ala Lys Lys Gly Gly Lys Ile Ala Val			
212	540	545	550	
214	gcttggatcc aatcaaccc tcggattacaa aatttgtgaa agattgactg gtattcttaa	2943		
216	ctatgttgct ccttttacgc tatgtggata cgctgcttta atgccttgt atcatgctat	3003		
218	tgcttcccgt atggctttca ttttctcctc ctgttataaaa tcctgggtgc tgtctctta	3063		
220	tgaggagttg tggcccggttgc tcaggcaacg tggcgtggtg tgcactgtgt ttgctgacgc	3123		
222	aaccccccact ggttggggca ttgccaccac ctgtcagctc ctttccggga ctttcgctt	3183		
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228	atggctgctc gcctgtgttgc ccacctggat tctgcgcggg acgtccttct gctacgtccc	3363		
230	ttcggccctc aatccagcgg accttccttc cccggcctgc ctgcccgtc tgcggcctct	3423		
232	tccgcgtctt cgagatctgc ctcgactgtg cttcttagtt gccagccatc ttttgttgc	3483		
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236	aatgaggaaa ttgcatcgca ttgtctgagt aggtgtcatt ctattctggg ggggtgggtg	3603		
238	gggcaggaca gcaaggggga ggattggaa gacaatagca ggcatgctgg ggactcgagt	3663		
240	taagggcgaa ttcccgatta ggatcttcct agagcatggc tacgtagata agtagcatgg	3723		
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244	cgctcgctcg ctcaactgagg cccggcgacc aaaggtcgcc cgacgcccgg gctttggcc	3843		
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250	tcccccttc gccagctggc gtaatagcga agaggccgc accgatcgcc cttcccaaca	4023		
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254	tgtgggtggtt acgcmcagcg tgaccgctac acttgccagc gccctagcgc ccgctccctt	4143		
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258	ggggctccct ttagggttcc gattnagtgc ttacggcac ctcgacccca aaaaacttga	4263		
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292	acttactcta gcttcccggc aacaattaat agactggatg gaggcggata aagttgcagg	5283		
294	accacttctg cgctcgcccc ttccggctgg ctggtttatt gctgataat ctggagccgg	5343		
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306	cgtagaaaaag	atcaaaggat	cttcttgaga	tcctttttt	ctgcgcgtaa	tctgctgctt	5703										
308	gcaaacaaaaa	aaaccaccgc	taccagcggt	ggtttgttg	ccggatcaag	agctaccaac	5763										
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312	gtagccgtag	ttaggccacc	acttcaagaa	ctctgttagca	ccgcctacat	acctcgctct	5883										
314	gctaattctg	ttaccagtgg	ctgctgccag	tggcgataag	tcgtgtctta	ccgggttgga	5943										
316	ctcaagacga	tagttaccgg	ataaggcgca	gcggtcgggc	tgaacggggg	gttcgtgcac	6003										
318	acagcccagc	ttggagcgaa	cgacacctac	cgaactgaga	tacctacagc	gtgagctatg	6063										
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324	tgtcggttt	cgcacactct	gacttgagcg	tcgattttg	tgatgctcg	cagggggcg	6243										
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328	tttgctcac	atgttcttc	ctgcgttatac	ccctgattct	gtggataacc	gtattaccgc	6363										
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353	Tyr	Ala	Leu	Val	Pro	Gly	Thr	Ile	Ala	Phe	Thr	Asp	Ala	His	Ile	Glu	
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374					115				120							125	
377	Ser	Lys	Lys	Gly	Leu	Gln	Lys	Ile	Leu	Asn	Val	Gln	Lys	Lys	Leu	Pro	
378					130				135							140	
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/15/2005
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Input Set : N:\efs\10604340A_efs\RNAi_seq_ST25.txt
Output Set: N:\CRF4\07152005\J604340A.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12

OK

VERIFICATION SUMMARY

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